

### AMENDMENTS TO THE CLAIMS

1. **(Currently amended)** A screening and/or quantification method of one or more transcriptional factors(s) present in a cell or cell lysate, said method comprising the steps of:

a. ~~\_\_\_\_\_~~ (a) binding to an insoluble solid support double-stranded DNA sequence(s) at the concentration of at least 0.01 pmole/cm<sup>2</sup> of said solid support surface, wherein the solid support is an array bearing at least 4 spots/cm<sup>2</sup> of solid support surface, each spot containing double-stranded DNA sequence(s) for the binding of transcriptional factor(s), said double-stranded DNA sequence comprising a specific sequence, said specific sequence being able to bind said one or more transcriptional factor(s) and said double-stranded DNA sequence being connected to the surface of the solid support by a spacer wherein said spacer is corresponding to or comprising at least a double-stranded DNA nucleotide sequence of between about 50 and about 250 base pairs, or wherein the spacer comprises a double-stranded DNA nucleotide sequence of between about 50 and about 250 base pairs;

b. ~~\_\_\_\_\_~~ (b) putting into contact said one or more transcriptional factor(s) with said bound double-stranded DNA sequence(s); and

e. ~~\_\_\_\_\_~~ (c) identifying and/or quantifying a signal resulting from the binding of said transcriptional factor(s) upon said double-stranded DNA sequence(s).

2. **(Original)** The method according to claim 1, wherein the transcriptional factor is present in solution at concentration lower than 20 nmolar (nM).

3. **Canceled**

4. **(Currently amended)** The method according to claim 1, wherein the signal resulting from the binding of the transcriptional factor upon the double-stranded DNA sequence is a non-radioactive ~~resulting~~ signal.

5. **(Previously presented)** The method according to claim 1, wherein the signal resulting from the binding of the transcriptional factor upon the double-stranded DNA sequence is obtained through an enzymatic reaction.

6. **(Previously presented)** The method according to claim 1, for the screening and/or quantification of multiple different transcriptional factors present in a same biological sample.

7. **(Previously presented)** The method according to claim 1, for the screening and/or quantification of transcriptional factors selected from the group consisting of NF-KB, AP-1, CREB, SP-1, C/EBP, GR, HIF-1, Myc, NF-AT, Oct, TBP, CBF-1 and factors listed in table 1.

8. **(Previously presented)** The method according to claim 1, for the screening and/or quantification of multiple different transcriptional factors upon a same support upon the same multiwell plate.

9-11. **Cancelled**

12. **(Previously presented)** The method according to claim 1, wherein the binding of the double-stranded DNA sequence(s) to the insoluble solid support is of non-covalent type and includes a binding pair comprising a first member and a second member, said first member being bound to the double-stranded DNA sequence, said second member being bound to the surface of the solid support.

13. **(Original)** The method according to claim 1, wherein the double-stranded DNA sequence(s) are covalently bound to the surface of the insoluble solid support.

14. **(Currently amended)** The method according to claim 1, wherein the double-stranded DNA specific sequence ~~is comprises repeated specific sequences on the same molecule.~~

15. **(Previously presented)** The method according to claim 1, wherein the double-stranded DNA sequences fixed on the support surface contain in part or totally one or several of the specific DNA sequences presented in the table 1.

16. **(Currently amended)** A screening and/or quantification method of one or more transcriptional factors(s) present in a cell or cell lysate, said method comprising the steps of:

a. ~~—~~(a) binding to an insoluble solid support double-stranded DNA sequence(s) at the concentration of at least 0.01 pmole/cm<sup>2</sup> of said solid support surface, wherein the solid support is an array bearing at least 4 spots/cm<sup>2</sup> of solid support surface, each spot containing double-stranded DNA sequence(s) for the binding of transcriptional factor(s), said double-stranded DNA sequence comprising a specific sequence, said specific sequence being able to bind said one or more transcriptional factor(s) and said double-stranded DNA sequence being connected to the surface of the solid support by a

spacer ~~wherein said spacer is corresponding to or comprising at least a~~ double-stranded DNA nucleotide sequence of between about 50 and about 250 base pairs, ~~or wherein the spacer comprises a double-stranded DNA nucleotide sequence of between about 50 and about 250 base pairs;~~

b. ~~—~~(b) putting into contact said one or more transcriptional factor(s) with said bound double-stranded DNA sequence(s); and

e. ~~—~~(c) identifying and/or quantifying a signal resulting from the binding of said transcriptional factor(s) upon said double-stranded DNA sequence(s), wherein said transcriptional factor is the HIV integrase.

17. **(Currently amended)** The method according to claim 1, comprising the step of ~~identification of~~ identifying at least one characteristic specific of the transcriptional factor activation.

18. **(Original)** The method according to claim 1, which comprises the steps of screening, quantifying and/or recovering compounds able to bind to said transcriptional factor(s) or inhibit the binding of transcriptional factor(s) to the specific sequence upon the double-stranded DNA sequence(s) bound to said solid support.

19. **(Currently amended)** The method according to claim 1, which further comprises prior to step (b) the steps-step of screening, quantifying and/or recovering contacting said cells with a candidate compound compounds which modulate is being evaluated to determine whether it modulates the binding and/or the activity of the said transcriptional factor(s) when they are put in contact with cells, tissues or organisms.

20. **(Currently amended)** The method according to claim 1, which further comprises prior to step (b) the steps-step of screening, quantifying and/or recovering contacting said cells with a candidate compound compounds which modulate is being evaluated to determine whether it modulates the activity of enzyme(s) or protein(s) acting on transcriptional factor(s), and then assayed for the binding to and/or activity of said transcriptional factor(s).

21. **(Currently amended)** A method according to claim 1, which further comprises the step of identifying ~~identification of~~ transcriptional factor(s) and/or of peptides which are part of ~~their~~ the transcriptional factor(s) active complex.

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22. **(Currently amended)** The method according to claim 1, which comprises the step of adding in the cell lysate an externally added transcriptional factor or a compound which is able to bind to the ~~eonsensus~~consensus-specific sequence.

23-33. **Cancelled**

34. **(Previously presented)** The method of Claim 12, wherein said binding pair is biotin/streptavidin.

35. **Cancelled**

36. **(Previously presented)** The method according to claim 12, wherein the binding pair is selected from the group consisting of biotin/streptavidin, hapten/receptor and antigen/antibody binding pair.

37. **(Previously presented)** The method according to claim 1, wherein step b) comprises putting into contact said one or more transcriptional factor(s) in a cell lysate with said bound double-stranded DNA sequence(s).

38. **Cancelled**